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GmmoriAe GmmoriAc		 CTACGG TTGTCTACGG	
GmmoriAe GmmoriAc		 AAATGAAGTT AAATGAA <u>T</u> TT	 TTCTTCATAA TTCTTCAT <u>G</u> A
GmmoriAe GmmoriAc		 TTTATAGGGT TTTATAGGGT	
GmmoriAe GmmoriAc		 GAAGGGAGGA GAAGGGAGGA	
GmmoriAe GmmoriAc		 GTACAGCGCA GTACAGCGCA	
GmmoriAe GmmoriAc		 AACCAAAAAT AACCAAAAAT	
GmmoriAe GmmoriAc		 ATGTTGCAAA ATGTTGCAAA	
GmmoriAe GmmoriAc	TAAAATATTT TAAAATATTT		

Figure 1

GmmoriAe GmmoriAc	1 MKFTGIFFII M <u>N</u> FTGIFF <u>M</u> I	 	AIKKGGKAIG AIKKGGKAIG	
	51 TAHDVYEHIK TAHDVYEHIK			

Figure 2

Figure 3

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1	GTAACAGTACCACCGTGTACAGTCGCAGTAGTTAGTCTTCAATCTTAGTGAAAACTTCGC
61	TTCTCTTTATCAACCATGAAGCTGACCGGTCTATTTTTCATGATCATGGCG \underline{A} TGCTCGCC Met $LysLeuThrGlyLeuPhePheMetIleMetAlaMetLeuAla$ Val
121	CTGTTTGTTGGCGCTGGTCAAGCCGACCCTAAGGTGCCCATTGGCGCCATCAAGAAGGGT LeuPheValGlyAlaGlyGlnAlaAspProLysValProlleGlyAlaIleLysLysGly
181	GGCAAAATTATTAAAAAAAGGTCTTGGTGTAATTGGTGCCGCTGGTACAGCGCATGAAGTA GlyLysIleIleLysLysGlyLeuGlyVallleGlyAlaAlaGlyThrAlaHisGluVal
241	TATAGCCACGTCAAGAACAGGCATTAGATTCTTGAAGAATATATAGTATATAATTATGAA <u>TyrSer</u> HisValLysAsnArgHis***
301	${\tt GTACTATCCTTTTGTATATGTGACTAAGTGCATAATGTAAAGTCAAATGAA} {\tt ATATATTT}$
361	ATTTATCCTCGTGCC
	Figure 5
1	ACTTCATTGTGTACAGTTGCAGGACTTAATACTTAGTGAACTACTTACT
61	${\tt ACCATGAAGCTGACCGGTCTATTTCTCATGATCATGGCGGTGCTCGCGCTGTTTGTT$
121	GCTGGTCAAGCCGACCCTAAGGTGCCCATTGGCGCTATCAAGAAGGGCGGCAAAATTATT AlaGlyGlnAlaAspProLysValProlleGlyAlaIleLysLysGlyGlyLysIleIle
181	AAAAAGGGTCTAGGTGTTGGCGCGCGGGCACAGCGCACGAAGTGTACAACCACGTT LysLysGlyLeuGlyValLeuGlyAlaAlaGlyThrAlaHisGluValTyrAsnHisVal
241	AGGAACAGGCAGTAACGTCATGCGTGATTGTTGTACATACA
301	TCTTGGCTGTGATATATCTTTAGATAAATTAATTTATAATACCACATACTTATTAGTAAA
361	ATACTCAAATATTGATTATAGATACATTAATAAATATTAATTA
421	TTTATGTACAATGCGAATAGATTCTACCCTCTGCCTCGTGCC

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GmmoriC1 GmmoriC2	GTAACAGTACCACCGTGTACAGTCGCAGTAGTTAGTCTTCAATCTTAGTGAAAACTTCGCACTTCATTGTGTACAGTTGCAGGACTTAATACTTAGTGAACTACTTAC	60 48
GmmoriC1 GmmoriC2	${\tt TTCTCTTTATCAACC} {\tt ATG} {\tt AAGCTGACCGGTCTATTTTCATGATCATGGCGATGCTCGCC} \\ {\tt TCCTCGTTACCAACC} {\tt ATG} {\tt AAGCTGACCGGTCTATTT} \underline{{\tt C}} {\tt TCATGATCATGGCG} \underline{{\tt G}} {\tt TGCTCGC} \underline{{\tt G}} \\$	120 108
GmmoriC1 GmmoriC2	$\tt CTGTTTGTTGGCGCTGGTCAAGCCGACCCTAAGGTGCCCATTGGCGCCATCAAGAAGGGTCTGTTTGTT$	180 168
GmmoriC1 GmmoriC2	$\tt GGCAAAATTATTAAAAAAGGTCTTGGTGTAATTGGTGCCGCTGGTACAGCGCATGAAGTAGGCAAAATTATTAAAAA\underline{G}GGTCT\underline{A}GGTGT\underline{G}CTTGG\underline{C}GCC\underline{G}GG\underline{C}ACAGCGC\underline{A}CGAAGT\underline{G}$	240 228
GmmoriC1 GmmoriC2	$\texttt{TATAGCCACGTCAAGAACAGGCAT} \textbf{TAGA} \texttt{ATTCTTGAAGAATATATAGTATATA}. \texttt{ATTA} \texttt{T} \texttt{TA\underline{C}A} \underline{\texttt{A}} \texttt{CCACGT} \underline{\texttt{T}} \underline{\texttt{A}} \underline{\texttt{G}} \texttt{GAACAGGCA} \underline{\texttt{G}} \textbf{TAA} \texttt{CGTCATGCGTGAT}. \texttt{TGTTGTACATACAGTACTT}$	297 287
GmmoriC1 GmmoriC2	${\tt GAAGTACTATCC.TTTTGTATATGTGAC.TAAGTGCATAATGTAAAGTCAAATGAAATATACCACATACGATTTGTCTTGGCTGTGATATATCTTTAGATAAATTAATT$	355 347
GmmoriC1 GmmoriC2	ATATTATTTATCCTCGTGCC 375 ACTTATTAGTAAAATACTCAAATA 462	

Figure 7

GmmoriC1	MKLTGLFFMIMAMLALFVGAGQADPKVPIGAIKKGGKIIKKGLGVIGAAG
GmmoriC2	MKLTGLF <u>L</u> MIMA <u>V</u> LALFVGAGQADPKVPIGAIKKGGKIIKKGLGV <u>L</u> GAAG
02	TAHEVYSHVKNRH TAHEVY \underline{N} HV \underline{R} NR \underline{Q}

Figure 8

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Bmmor	MNILKFFFVFIVAMSLVSCS-TAAPAKIPIKAIKTVGKAVGKGLRAINIASTANDVFNFLKPKKRKH-
Hpmor	AMSLVSCS-TAAPAKIPIKAIKTVGKAVGKGLRAINIASTANDVFNFLKPKKRKH-
Hvvir	GKIPIGAIKKAGKAIGKGLRAVNIASTAHDVYTFFKPKKR-H-
Slmor	MKLTKVFVILIVVVALLVPS-EAAPGKIPVKAIKKAGAAIGKGLRAINIASTAHDVYSFFKPKHKKKH
Semor	MKLTKVFVIVIVVVALLVPS-EAAPGKIPVKAIKKAGTAIGKGLRAINIASTAHDVYSFFKPKHKKKH
Msmor	MKLTSLFIFVIVALSLLFSSTDAAPGKIPVKAIKQAGKVIGKGLRAINIAGTTHDVVSFFRPKKKKH-
CiP1647	ASRAWRALDLASTAYDIASIFNRKRE-
CiP1648	GKIPVEALKKGAKVAGRAWRALDLASTAYDIAHLFDRKRN-
CiP1646	GKIPINAIRKGAKAVGHGLRALNIASTAHDIASAFHRKRKH
GmmoriB	MRLSIILVVVMMVMAMFVSSGDAAPGKIPVKAIKKGGQIIGKALRGINIASTAHDIISQFKPKKKKNH
GmmoriC1	MKLTGLFFMIMAMLALFVGAGQADP-KVPIGAIKKGGKIIKKGLGVIGAAGTAHEVYSHVKNRH
GmmoriC2	MKLTGLFLMIMAVLALFVGAGQADP-KVPIGAIKKGGKIIKKGLGVLGAAGTAHEVYNHVRNRQ
BmmorX	MYFLKYFIVVLVALSLMICSGQADP-KIPVKSLKKGGKVIAKGFKVLTAAGTAHEVYSHVRNRGNQG-
GmmoriA	MKFTGIFFIIMAIIALFIGSNEAAP-KVNVNAIKKGGKAIGKGFKVISAASTAHDVYEHIKNRRH

Figure 9